



ggcacgagga gatctaggtt caaattaatg ttgccctag tggtaaagga cagagaccct 60
 cagactgatg aaatgcgctc agaattactt agacaaagcg gatatttgcc actctcttcc 120
 ccttttctcg tgtttttgta gtgaagagac ctgaaagaaa aaagtaggga gaacataatg 180
 agaacaaata cggtaatctc ttcatttgct ag ttcaagtg ctggacttgg gacttaggag 240
 gggcaatgga gccgcttagt gcctacatct gacttggact gaaatatagg tgagagacaa 300
 gattgtctca tatccgggga aatcataacc tatgactagg acgggaagag gaagcactgc 360
 ctttacttca gtgggaatct cggcctcagc ctgcaagcca agtggttcaca gtgagaaaag 420
 caagagaata agctaatact cctgtcctga acaaggcagc ggctccttgg taaagctact 480
 ccttgatcga tcctttgcac cggattgttc aaagtggacc ccaggggaga agtcggagca 540
 aagaacttac caccaagcag tccaagaggc ccagaagcaa ac ctg gag gtg aga 594
 Met Glu Val Arg

1

ccc aaa gaa agc tgg aac cat gct gac ttt gta cac tgt gag gac aca 642
 Pro Lys Glu Ser Trp Asn His Ala Asp Phe Val His Cys Glu Asp Thr
 5 10 15 20

gag tct gtt cct gga aag ccc agt gtc aac gca gat gag gaa gtc gga 690
 Glu Ser Val Pro Gly Lys Pro Ser Val Asn Ala Asp Glu Glu Val Gly
 25 30 35

ggc ccc caa atc tgc cgt gta tgt ggg gac aag gcc act ggc tat cac 738
 Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala Thr Gly Tyr His
 40 45 50

ttc aat gtc atg aca tgt gaa gga tgc aag ggc ttt ttc agg agg gcc 786
 Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ala
 55 60 65

atg aaa cgc aac gcc cgg ctg agg tgc ccc ttc cgg aag ggc gcc tgc 834
 Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg Lys Gly Ala Cys
 70 75 80

gag atc acc cgg aag acc cgg cga cag tgc cag gcc tgc cgc ctg cgc 882
 Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala Cys Arg Leu Arg
 85 90 95 100

aag tgc ctg gag agc ggc atg aag aag gag atg atc atg tcc gac gag 930
 Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile Met Ser Asp Glu
 105 110 115

gcc gtg gag gag agg cgg gcc ttg atc aag cgg aag aaa agt gaa cgg 978
 Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys Lys Ser Glu Arg
 120 125 130

aca ggg act cag cca ctg gga gtg cag ggg ctg aca gag gag cag cgg 1026
 Thr Gly Thr Gln Pro Leu Gly Val Gln Gly Leu Thr Glu Glu Gln Arg
 135 140 145

atg atg atc agg gag ctg atg gac gct cag atg aaa acc ttt gac act 1074
 Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys Thr Phe Asp Thr
 150 155 160

acc ttc tcc cat ttc aag aat ttc cgg ctg cca ggg gtg ctt agc agt 1122
 Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly Val Leu Ser Ser
 165 170 175 180

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FIG. 1A-1

ggc tgc gag ttg cca gag tct ctg cag gcc cca tcg agg gaa gaa gct	1170
Gly Cys Glu Leu Pro Glu Ser Leu Gln Ala Pro Ser Arg Glu Glu Ala	
185 190 195	
gcc aag tgg agc cag gtc cgg aaa gat ctg tgc tct ttg aag gtc tct	1218
Ala Lys Trp Ser Gln Val Arg Lys Asp Leu Cys Ser Leu Lys Val Ser	
200 205 210	
ctg cag ctg cgg ggg gag gat ggc agt gtc tgg aac tac aaa ccc cca	1266
Leu Gln Leu Arg Gly Glu Asp Gly Ser Val Trp Asn Tyr Lys Pro Pro	
215 220 225	
gcc gac agt ggc ggg aaa gag atc ttc tcc ctg ctg ccc cac atg gct	1314
Ala Asp Ser Gly Gly Lys Glu Ile Phe Ser Leu Leu Pro His Met Ala	
230 235 240	
gac atg tca acc tac atg ttc aaa ggc atc atc agc ttt gcc aaa gtc	1362
Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser Phe Ala Lys Val	
245 250 255 260	
atc tcc tac ttc agg gac ttg ccc atc gag gac cag atc tcc ctg ctg	1410
Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu	
265 270 275	
aag ggg gcc gct ttc gag ctg tgt caa ctg aga ttc aac aca g tg ttc	1458
Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe Asn Thr Val Phe	
280 285 290	
aac gcg gag act gga acc tgg gag tgt ggc cgg ctg tcc tac tgc ttg	1506
Asn Ala Glu Thr Gly Thr Trp Glu Cys Gl y Arg Leu Ser Tyr Cys Leu	
295 300 305	
gaa gac act gca ggt ggc ttc cag caa ctt cta ctg gag ccc atg ctg	1554
Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu Glu Pro Met Leu	
310 315 320	
aaa ttc cac tac atg ctg aag aag ctg cag ctg cat gag gag gag tat	1602
Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His Glu Glu Glu Tyr	
325 330 335 340	
gtg ctg atg cag gcc atc tcc ctc ttc tcc cca gac cgc cca ggt gtg	1650
Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp Arg Pro Gly Val	
345 350 355	
ctg cag cac cgc gtg gtg gac cag ctg cag gag caa ttc gcc att act	1698
Leu Gln His Arg Val Val Asp Gln Leu Gln Glu Gln Phe Ala Ile Thr	
360 365 370	
ctg aag tcc tac att gaa tgc aat cgg ccc cag cct gct cat agg ttc	1746
Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro Ala His Arg Phe	
375 380 385	
ttg ttc ctg aag atc atg gct atg ctc acc gag ctc cgc agc atc aat	1794
Leu Phe Leu Lys Ile Met Ala Met Leu Thr Glu Leu Arg Ser Ile Asn	
390 395 400	

FIG. 1A-2

gct cag cac acc	cag cgg ctg ctg cgc atc	cag gac ata cac ccc ttt	1842
Ala Gln His Thr	Gln Arg Leu Leu Arg Ile	Gln Asp Ile His Pro Phe	
405	410	415	420
gct acg ccc ctc atg	cag gag ttg ttc ggt atc	aca ggt agc tga	1887
Ala Thr Pro Leu Met	Gln Glu Leu Phe Gly Ile	Thr Gly Ser	
425	430		
gtggctgtcc ttgggtgaca	cctccgagag gtagttagac	ccagagccct ctgagtcgcc	1947
actcccgggc caagacagat	ggacactgcc aagagccgac	aatgccctgc tggcctgtct	2007
ccctagggaa ttctgtctat	gacagctggc tagcattcct	caggaaggac atgggggtgcc	2067
c			2068

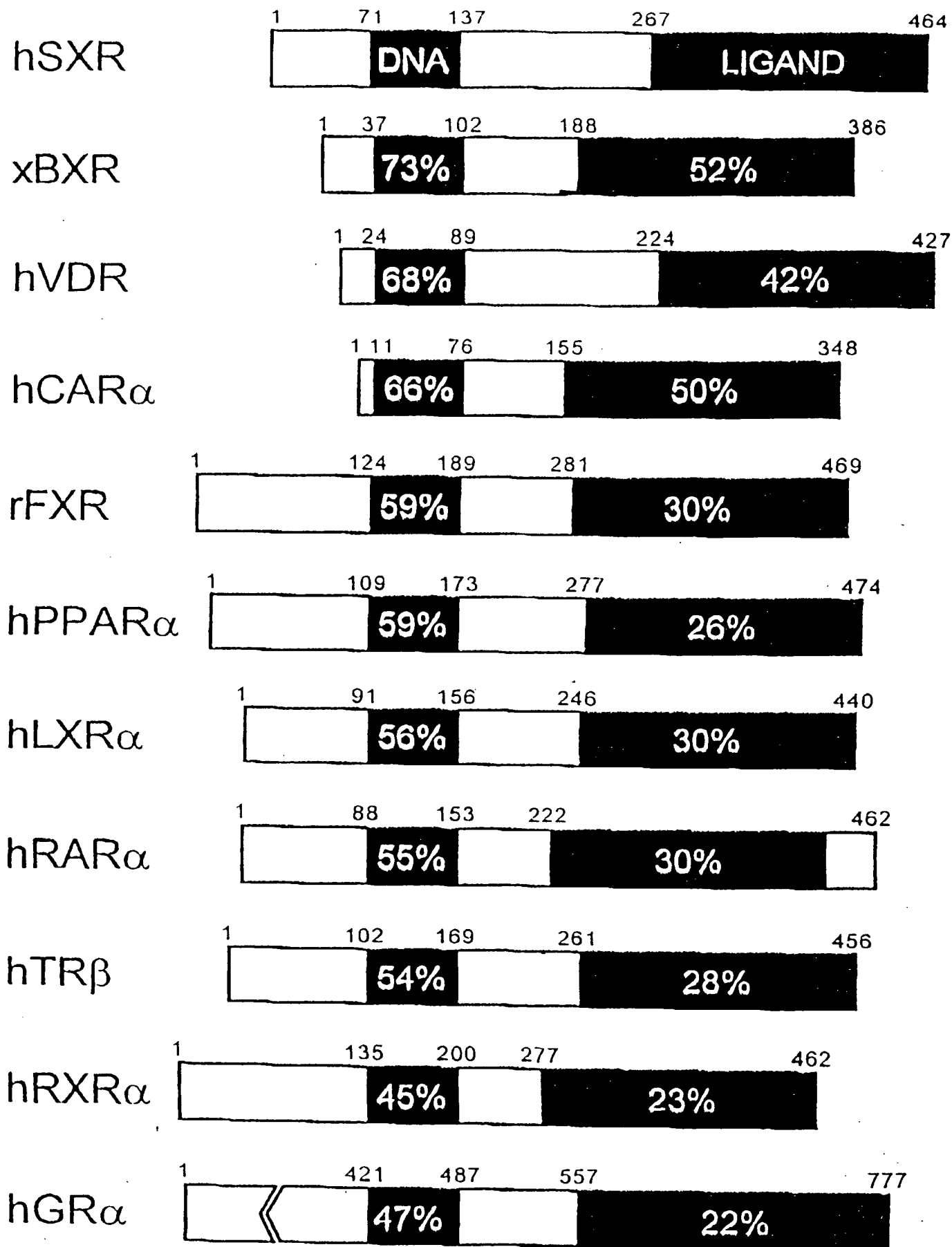


FIG. 1B

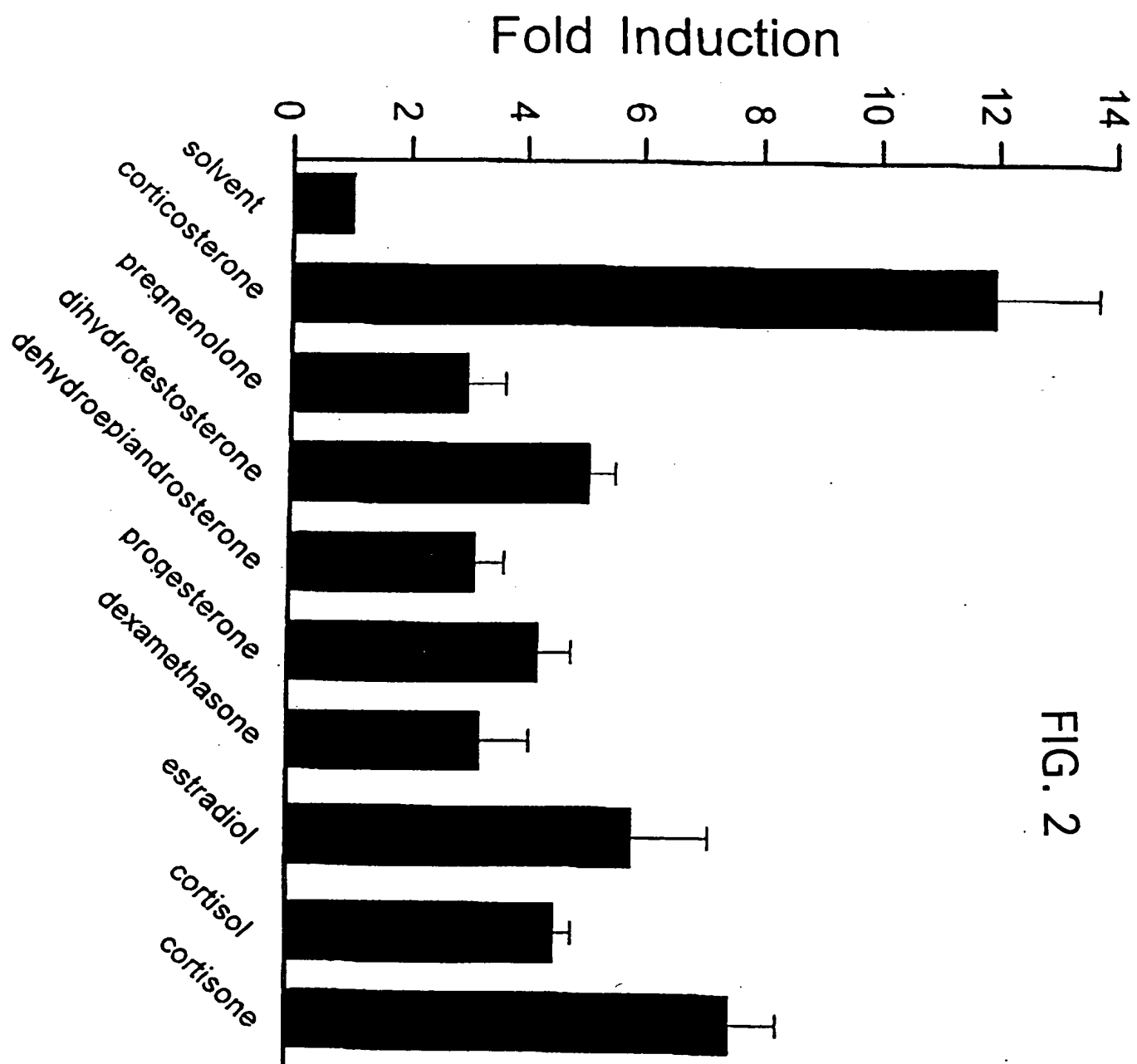


FIG. 2

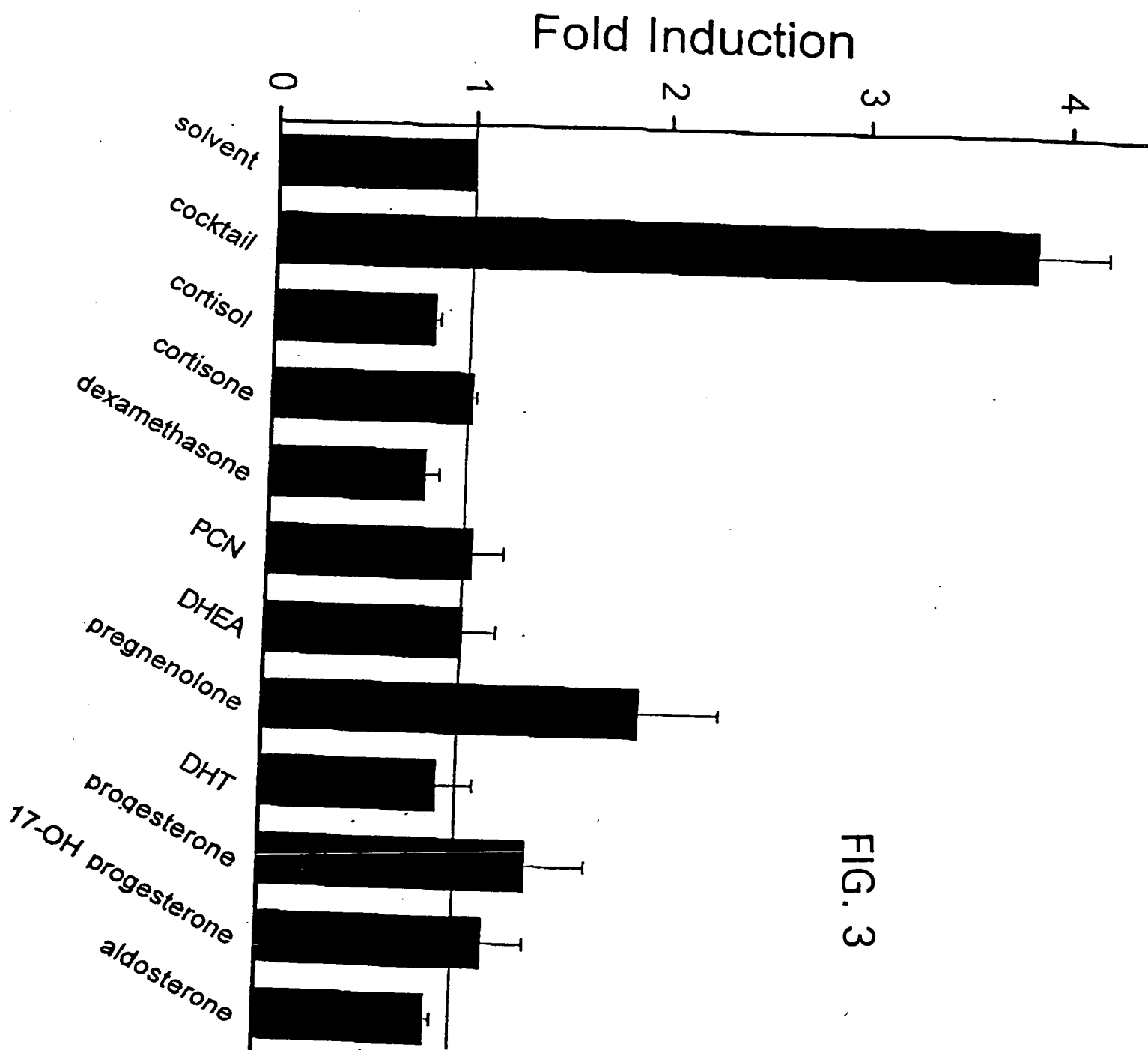


FIG. 3

14



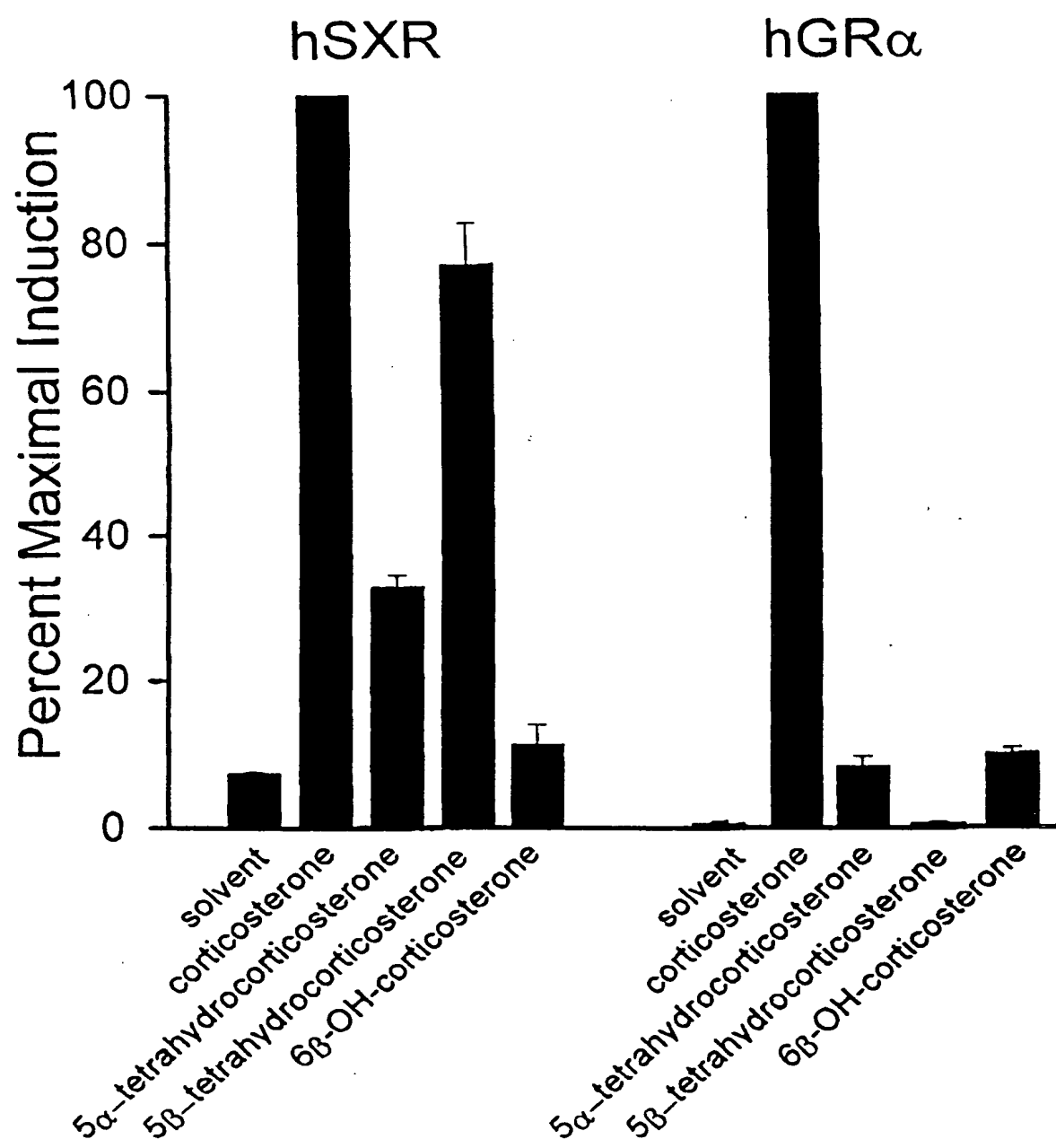


FIG 5

DR-3

rCYP3A1	tagac AGTTCA tga AGTTCA tctac
rCYP3A2	taagc AGTTCA taa AGTTCA tctac
rUGT1A6	actgt AGTTCA taa AGTTCA catgg

DR-4

rbCYP2C1	caatc AGTTCA acag GGTTCa ccaat
rP450R	cac AGGTGA gctg AGGCCA gcagc AGGTCG aaa

DR-5

rCYP2A1	gtgca GGTTCa actgg AGGTCA acatg
rCYP2A2	gtgct GGTTCa actgg AGGTCA gtatg
rCYP2C6	agtct AGTTCA gtggg GGTTCa gtctt
rCYP2E1	gagat GGTTCa aggaa GGTTCa ttaac

FIG. 6A

CYP3A4	tagaata TGAACt caaagg AGGTCA gtgagtgg
CYP3A5	tagaata TGAACt caaagg AGGTAA gcaaaggg
CYP3A7	tagaata TTAACt caatgg AGGC.A gtgagtgg

FIG. 6B

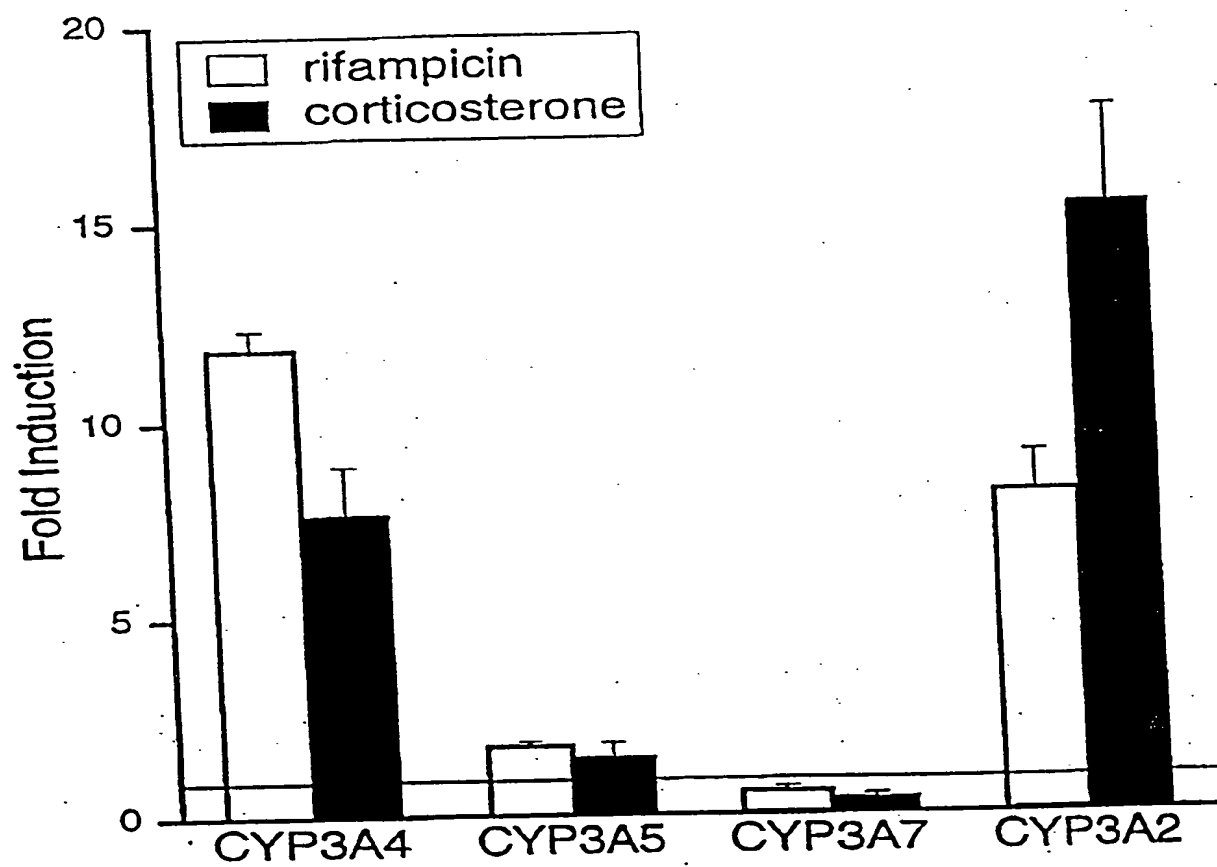
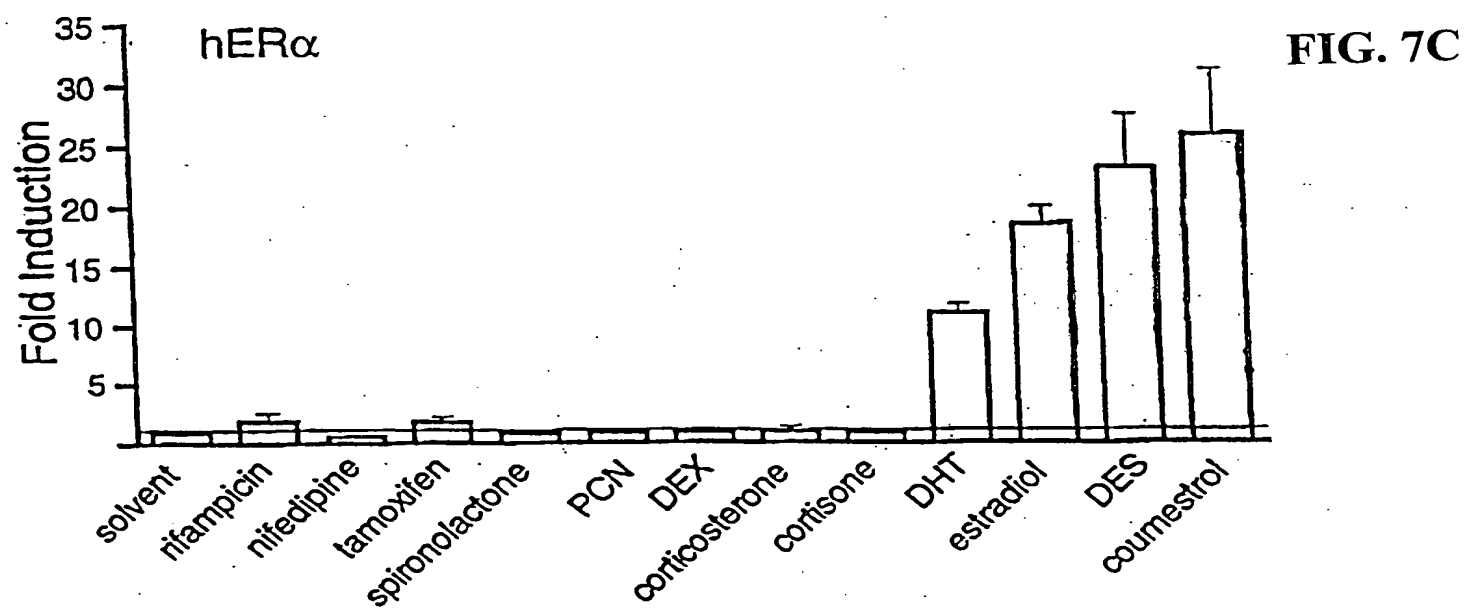
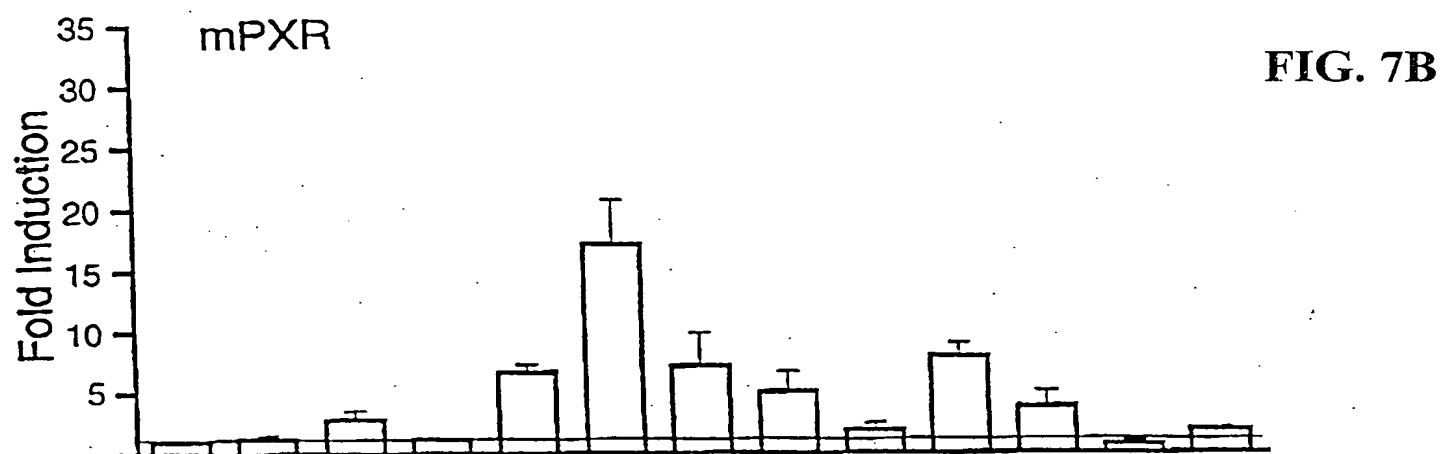
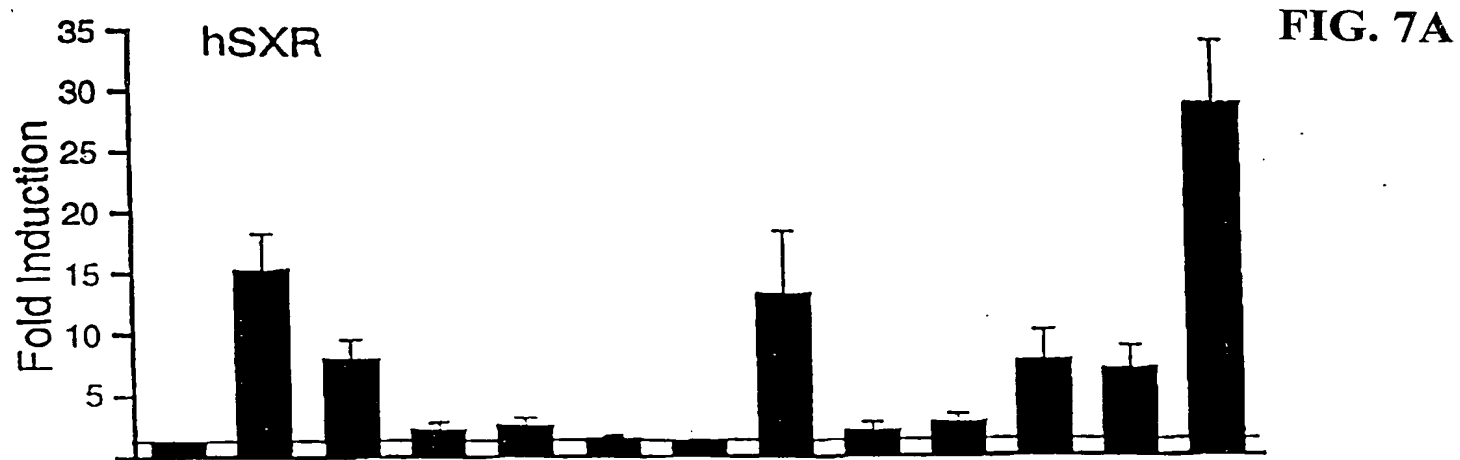


FIG. 6C



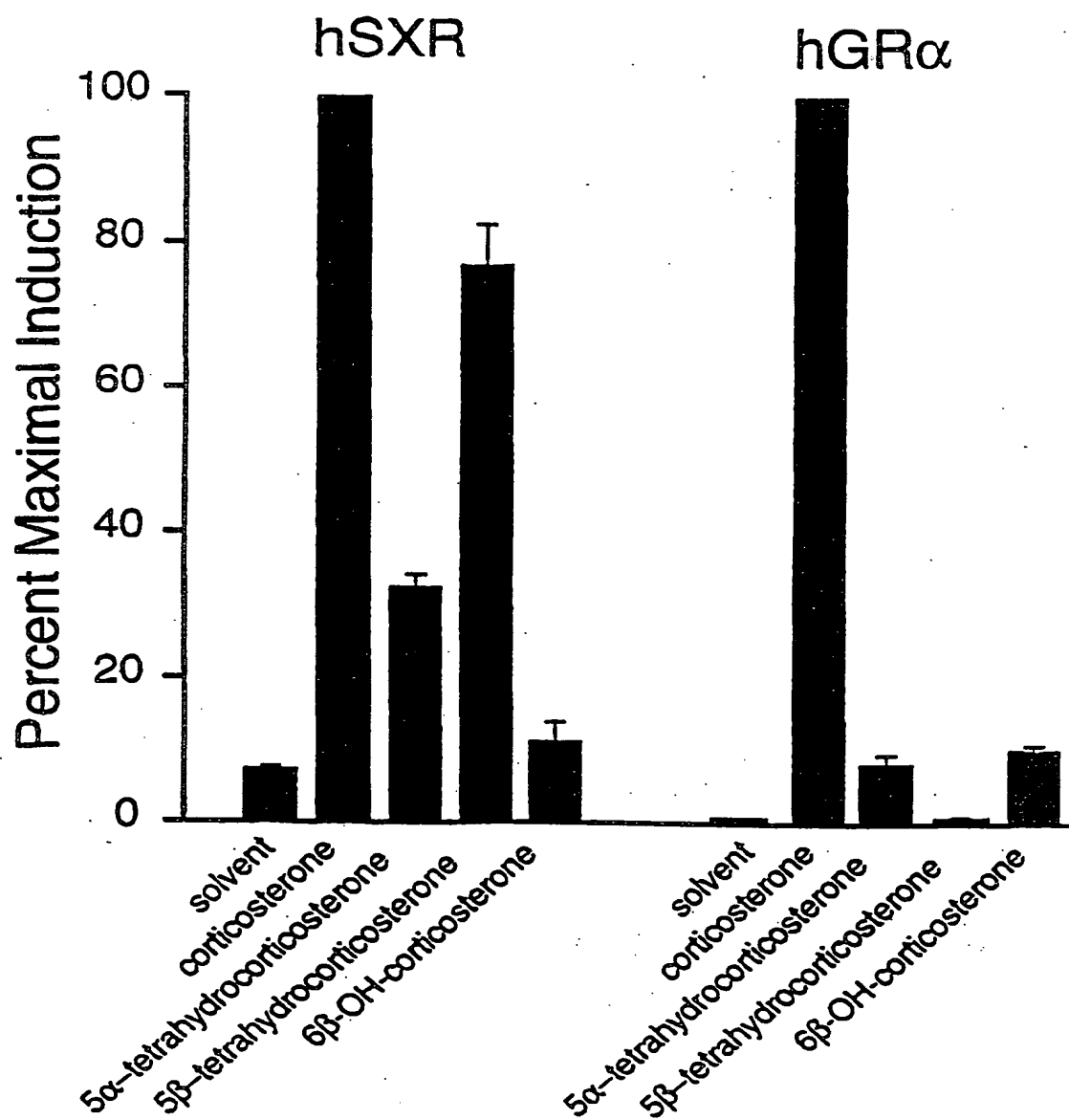


Figure 7D

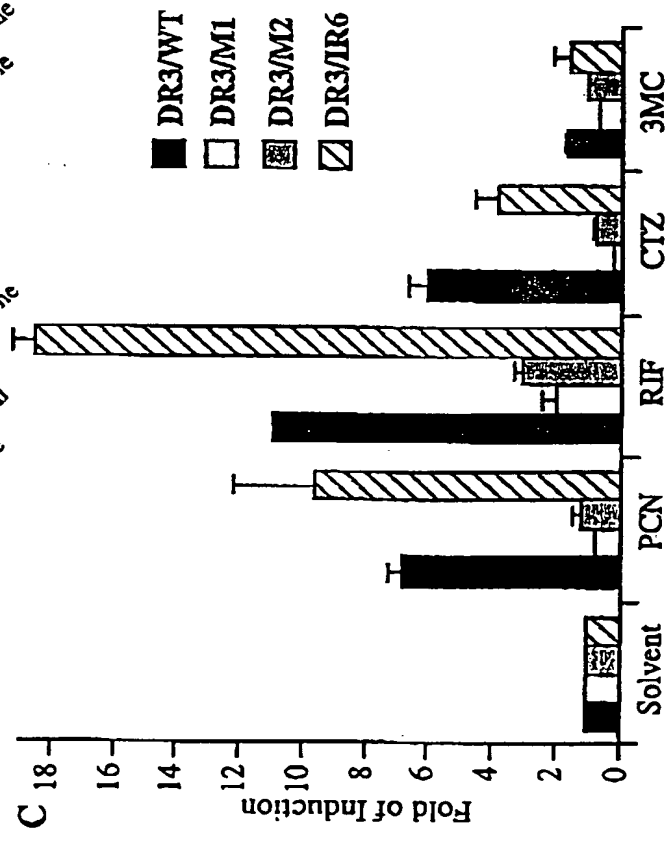
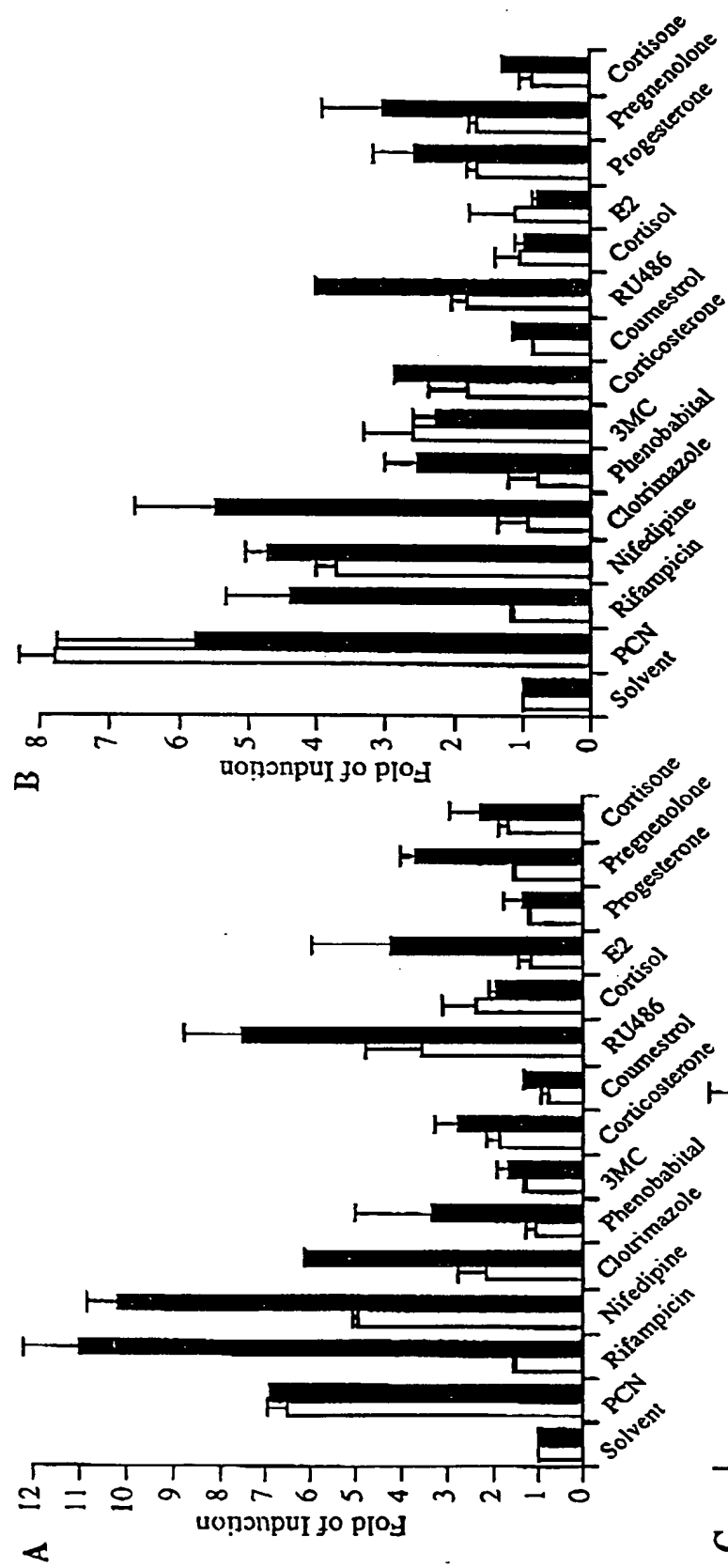


FIG. 8

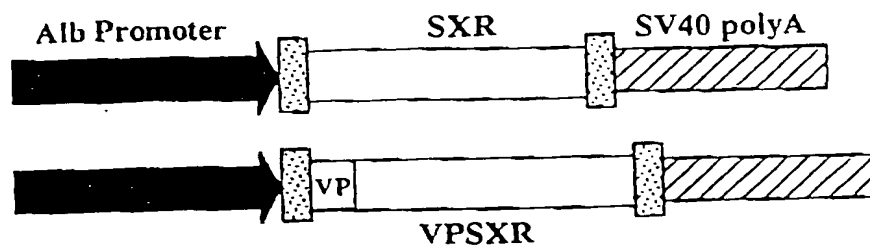


FIG. 9

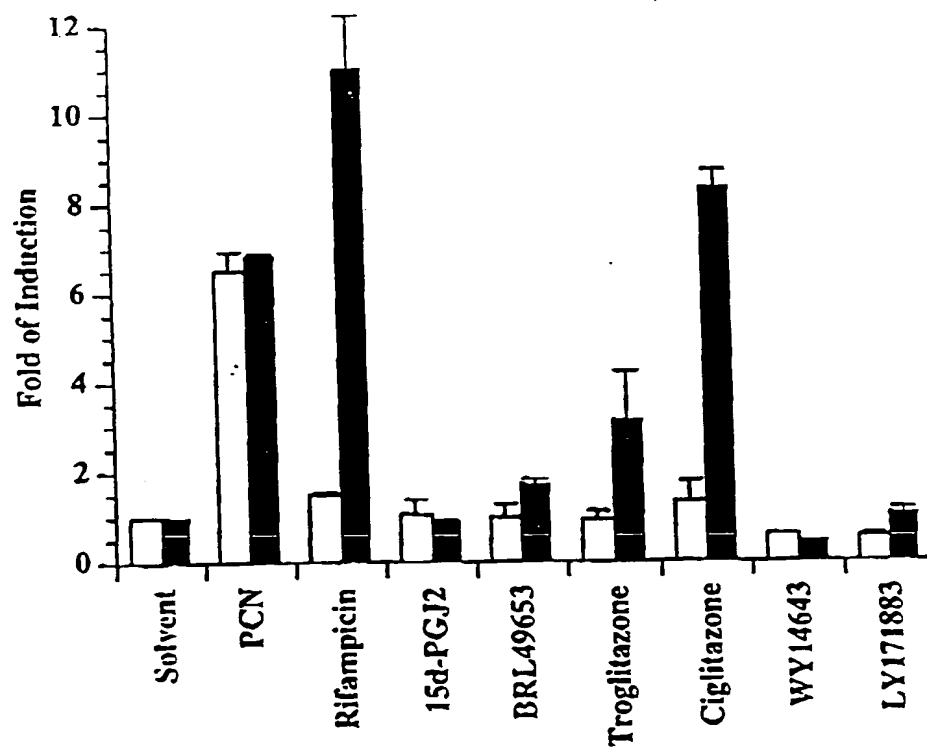


FIG. 10

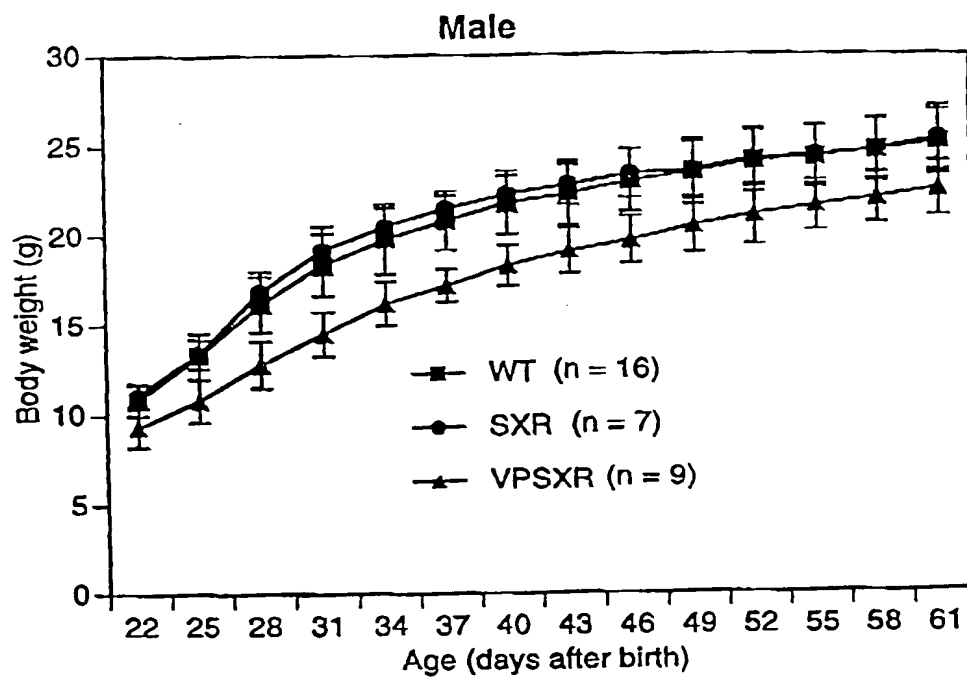


FIG. 11

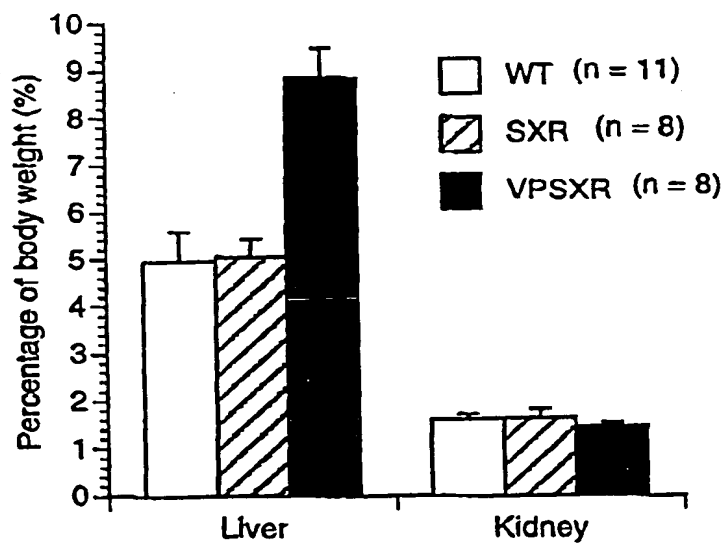


FIG. 12

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